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Om nucleic - nucleic search, using sw model

Run on: March 15, 2003, 12:16:13 : Search time 0.664702 Seconds

(without alignments) 9688.871 Million cell updates/sec

Title: US-08-978-217-13
Perfect score: 21
Sequence: 1 CCGGGACATCTCATCCACCC 21

Scoring table: IDENTITY_NIC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15333831 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
4: /cgn2_6/ptodata/1/ina/PCUS_COMB.seq: *
5: /cgn2_6/ptodata/1/ina/backtles1.seq: *

6: /cgn2_6/ptodata/1/ina/backtles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1
US-08-746-789A-1
Sequence 1, Application US/08746789A
; Patent No. 5789200
; GENERAL INFORMATION:
; APPLICANT: Ismail Kola, Martin J. Tymons, Christine DeBouck
; TITLE OF INVENTION: A No. 5789200el Human ETS Family Member, ELF3
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 SwedeLand Road, P.O. Box 1539
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM 486
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
; SOFTWARE: MICROSOFT WORD
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/746,789A
; FILING DATE: No. 5789200elember 15, 1996
; CLASSIFICATION: 514
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: William T. Han
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: ATG 50024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610 270 5219
; TELEFAX: 610 270 4026
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1920
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: No

US-08-746-789A-1
Query Match 100.0%; Score 21; DB 1; Length 1920;
Best Local Similarity 100.0%; Pred. No. 0.69; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qry 1 CCGGGACATCTCATCCACCC 21
Do 951 CCGGGACATCTCATCCACCC 971

RESULT ²
US-08-456-647B-1/c
Sequence 1, Application US/08456647B
; GENERAL INFORMATION:
; APPLICANT: Lemke Ph.D. et al., Greg E.
; TITLE OF INVENTION: PROTEIN-TYROSINE KINASE GENES
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,647B
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 530
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/237,401
; FILING DATE: 02-MAY-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/884,486
; FILING DATE: 15-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell Ph.D., John R.
; REFERENCE/DOCKET NUMBER: 31,678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 678-5099
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 165 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLSCULE TYPE: DNA
; IMMEDIATE SOURCE:
; CLEONE: Tyro-1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..165
; US-08-456-647B-1

RESULT ³
US-08-237-401A-1/c
Query Match 77.1%; Score 16.2; DB 1; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 2; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 3; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 4; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 5; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 6; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 7; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 8; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 9; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 10; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 11; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 12; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 13; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 14; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 15; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 16; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 17; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 18; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 19; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 20; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 21; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 22; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 23; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 24; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 25; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 26; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 27; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 28; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 29; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 30; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 31; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 32; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 33; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 34; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 35; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 36; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 37; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 38; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 39; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 40; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 41; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 42; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 43; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 44; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 45; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 46; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 47; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 48; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 49; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 50; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 51; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 52; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 53; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 54; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 55; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

Query Match 77.1%; Score 16.2; DB 56; Length 165;
Best local similarity 85.7%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; LOCATIONS: 1..165

RESULT ⁴
US-09-643-597-303
Sequence 303, Application US/09643597
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Ligun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Achell, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; AND DIAGNOSIS OF LUNG CANCER
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; CURRENT APPLICATION NUMBER: US/09/643,597
; FILE REFERENCE: 21121.455C11
; SSEQ ID NO: 303
; LENGTH: 361
; TYPE: DNA
; ORGANISM: Homo sapien

FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)..(361)
 OTHER INFORMATION: n = A, T, C or G

US-09-643-597-303

Query Match 77.1%; Score 16.2; DB 4; Length 361;
 Best Local Similarity 85.7%; Pred. No. 82; Mismatches 3; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCGGAGATCTCATCACC 21
 Db 257 CCGGGAGTCCCTCCCCACCC 277

RESULT 5
 US-09-328-111-567 Application US/09328111
 ; Sequence 567, Application US/09328111
 ; Patent No. 6262333
 ; GENERAL INFORMATION:
 ; APPLICANT: Endgege, Wilson O.
 ; APPLICANT: Steinmann, Kathleen E.
 ; APPLICANT: Astle, Jon H.
 ; APPLICANT: Burgess, Christopher C.
 ; APPLICANT: Bushnell, Steven B.
 ; APPLICANT: Carroll III, Eddie J.
 ; APPLICANT: Catino, Theodore J.
 ; APPLICANT: Derti, Adnan M.
 ; APPLICANT: Ford, Donna M.
 ; APPLICANT: Lewis, Marcia E.
 ; APPLICANT: Monahan, John E.
 ; APPLICANT: Schlegel, Robert
 ; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
 ; TITLE OF INVENTION: PRODUCTS
 ; FILE REFERENCE: CCD-257 (US)
 ; CURRENT APPLICATION NUMBER: US/09/328,111
 ; CURRENT FILING DATE: 1999-06-08
 ; EARLIER APPLICATION NUMBER: US 60/088,801
 ; EARLIER FILING DATE: 1998-06-10
 ; NUMBER OF SEQ ID NOS: 850
 ; SOFTWARE: FasleSEQ for Windows Version 3.0
 ; SEQ ID NO 567
 ; LENGTH: 427
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-328-111-567

Query Match 77.1%; Score 16.2; DB 4; Length 427;
 Best Local Similarity 85.7%; Pred. No. 83; Mismatches 0; Indels 3; Gaps 0;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCGGAGATCTCATCACC 21
 Db 257 CCGGGAGTCCCTCCCCACCC 277

RESULT 6
 US-08-826-246-9/c
 ; Sequence 9, Application US/08826246
 ; Patent No. 6048109
 ; GENERAL INFORMATION:
 ; APPLICANT: Faib, Dean
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
 ; TITLE OF INVENTION: THE TREATMENT AND DIAGNOSIS OF
 ; TITLE OF INVENTION: CARDIOVASCULAR DISEASE
 ; NUMBER OF SEQUENCES: 44
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: PENNIE & EDMONDS LLP
 ; STREET: 1155 Avenue of the Americas
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FasleSEQ Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/944,495
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 08/799,910
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 60/011,787
 ; FILING DATE: 16-FEB-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A.
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE DOCKET NUMBER: 7853-078-999
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212)7509090
 ; TELEFAX: (212)8699741
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1228 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: Coding Sequence
 ; LOCATION: 1..1468
 ; OTHER INFORMATION:
 ; US-08-826-246-9

Query Match 77.1%; Score 16.2; DB 3; Length 1228;
 Best Local Similarity 85.7%; Pred. No. 89; Mismatches 0; Indels 3; Gaps 0;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCGGAGATCTCATCACC 21
 Db 952 CCGGGAGTCCCTCCCCACCC 932

RESULT 7
 US-08-944-495-9/c
 ; Sequence 9, Application US/08944495
 ; Patent No. 6087477
 ; GENERAL INFORMATION:
 ; APPLICANT: Faib, Dean
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
 ; TITLE OF INVENTION: THE TREATMENT AND DIAGNOSIS OF
 ; TITLE OF INVENTION: CARDIOVASCULAR DISEASE
 ; NUMBER OF SEQUENCES: 44
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: PENNIE & EDMONDS LLP
 ; STREET: 1155 Avenue of the Americas
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FasleSEQ Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/944,495
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 08/799,910

; PRIOR APPLICATION NUMBER: 08/485,573
 ; PRIOR FILING DATE: 1998-06-07
 ; PRIOR APPLICATION NUMBER: 08/1386,844
 ; NUMBER OF SEQ ID NOS: 46
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 1228
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(468)
 ; US-09-288-292A-5

; RESULT 11
 ; Query Match 77.1%; Score 16.2; DB 4; Length 1228;
 ; Best Local Similarity 85.7%; Pred. No. 89; Mismatches 0; Indels 0; Gaps 0;
 ; Matches 18; Conservative
 ; QY 1 CCGGGACATCCATCCAC 21
 ; Db 952 CCGGAGCTCCAC 932

; RESULT 12
 ; US-09-129-033-1
 ; Sequence 1, Application US/09129033
 ; Patent No. 6229185
 ; GENERAL INFORMATION:
 ; APPLICANT: Kauppinen, Markus Sakari
 ; APPLICANT: Kofod, Lene Venke
 ; APPLICANT: Andersen, Lene No. 6329185b0e
 ; APPLICANT: Clausen, Ib Groth
 ; TITLE OF INVENTION: An Enzyme with Galactanase Activity
 ; FILE REFERENCE: 4685-204-US
 ; CURRENT APPLICATION NUMBER: US/09/129 033
 ; CURRENT FILING DATE: 1998-08-04
 ; PRIOR APPLICATION NUMBER: PCT/DK97/00091
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 1026
 ; TYPE: DNA
 ; ORGANISM: Meripilus giganteus
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(1026)
 ; US-09-129-033-1

; RESULT 13
 ; Query Match 72.4%; Score 15.2; DB 4; Length 1026;
 ; Best Local Similarity 85.0%; Pred. No. 2.4e+02; Mismatches 3; Indels 0; Gaps 0;
 ; Matches 17; Conservative
 ; QY 1 CCGGGACATCCATCCAC 20
 ; Db 552 CCGGAGATCCATCCAC 571

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/998,416
 ; FILING DATE: 24-DEC-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: CH 0016/97
 ; FILING DATE: 31-DEC-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Meigs, J. Timothy
 ; REGISTRATION NUMBER: 38,241
 ; REFERENCE/DOCKET NUMBER: PFI-5-30306/A/GCC1976
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 919-511-8557
 ; TELEFAX: 919-541-8689
 ; INFORMATION FOR SEQ ID NO: 682:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 718 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: Linear
 ; MOLECULE TYPE: DNA (genomic)
 ; ORIGINAL SOURCE:

; ; ORGANISM: PAG1452UP
 ; US-08-998-416-682
 ; Query Match 75.2%; Score 15.8; DB 4; Length 718;
 ; Best Local Similarity 89.5%; Pred. No. 1.3e+02; Mismatches 2; Indels 0; Gaps 0;
 ; Matches 17; Conservative
 ; QY 1 CCGGGACATCCATCCAC 19
 ; Db 162 CTGGACATCCATCCAC 180

; ; ORGANISM: Thauera aromatica
 ; US-09-516-914-16
 ; Query Match 72.4%; Score 15.2; DB 4; Length 1074;
 ; Best Local Similarity 85.0%; Pred. No. 2.4e+02; Mismatches 3; Indels 0; Gaps 0;
 ; Matches 17; Conservative
 ; QY 1 CCGGGACATCCATCCAC 20

Db 439 ||||||| ||||| ||||| CCGGGATGCCACATCCACC 420

RESULT 14

US-08-461-775-8

Sequence 8, Application US/08461775

PATENT NO. 5,858,773

GENERAL INFORMATION:

APPLICANT: MAZODIER, Philippe

APPLICANT: GUILLEM, Gerard

TITLE OF INVENTION: INITIATION OF TRANSCRIPTION

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Burns, Doane, Swecker & Mathis

STREET: George Mason Bldg., Washington & Prince Sts.

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/031,606

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/050,313

FILING DATE: 10-MAY-1993

APPLICATION NUMBER: FR 9011186

FILING DATE: 10-SEP-1990

FILING DATE: 10-SEP-1990

CLASSIFICATION:

NAME: Crane-Feury, Sharon E

REGISTRATION NUMBER: 36,113

REFERENCE/DOCKET NUMBER: 010830-035

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 1320 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 1..1320

US-09-031-606-8

Query Match 72.4%; Score 15.2; DB 2; Length 1320;

Best Local Similarity 85.0%; Pred. No. 2.5e+02;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCGGGACATCCATCCACC 20

Db 645 CCCGTACATCCGATCCACC 664

Search completed: March 15, 2003, 15:13:08

Job time : 9.6647 secs

RESULT 15

US-09-031-606-9

Sequence 8, Application US/09031606

PATENT NO. 6,153,404

GENERAL INFORMATION:

APPLICANT: MAZODIER, Philippe

APPLICANT: GUILLEM, Gerard

TITLE OF INVENTION: REGULATORY NUCLEOTIDE SEQUENCE OF THE

TITLE OF INVENTION: INITIATION OF TRANSCRIPTION

NUMBER OF SEQUENCES: 15

Qy 1 CCGGGACATCCATCCACC 20

Db 645 CCCGTACATCCGATCCACC 664

Query Match 72.4%; Score 15.2; DB 2; Length 1320;

Best Local Similarity 85.0%; Pred. No. 2.5e+02;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCGGGACATCCATCCACC 20

Db 645 CCCGTACATCCGATCCACC 664

Search completed: March 15, 2003, 15:13:08

Job time : 9.6647 secs